Exhibit 2

Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.17 [Aug-19-2007]

Matrix [BLOSUM62] gap open [11] gap extension: [1]
x_dropoff [0] expect [10.0000] wordsize: [3] Filter ☑ View option [Standard]
Masking character option [X for protein, n for nucleotide] Masking color option [Black]
☐ Show CDS translation   [Align]

Sequence 1: unnamed protein product
Length = 71 (1 .. 71)

Sequence 2: unnamed protein product
Length = 64 (1 .. 64)
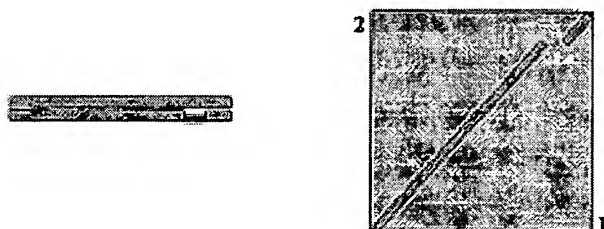
NOTE: Bitscore and expect value are calculated based on the size of the nr database.

```
Score =  100 bits (250),  Expect = 2e-20
Identities = 64/71 (90%), Positives = 64/71 (90%), Gaps = 7/71 (9%)

Query  1   MVLRQLSRKASVKVSKTNSGTKKRAQRILIFLLEFLLDFCTGEDSVDGRKRDRHSGLSEQ  60
           MVLRQLSRKASVKVSKTNSGTKKRAQRILIFLLEFLLDFCTGEDSVDGNKRDRHSG
Sbjct  1   MVLRQLSRKASVKVSKTNSGTKKRAQRILIFLLEFLLDFCTGEDSVDGNKRDRHSG----  56

Query  61  TYSALPEPKAT  71   SEQ ID NO: 1
           ALPEPKAT
Sbjct  57  ---ALPEPKAT  64   SEQ ID NO: 22
```

CPU time: 0.03 user secs.   0.01 sys. secs   0.04 total secs.